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OM protein - protein search, using sw model

Run on: December 27, 2005, 14:05:13 ; Search time 149.635 Seconds
(without alignments)
544,502 Million cell updates/sec

Title: US-10-811-508-9

Perfect score: 1013

Sequence: 1 MSRRNPCKFEIRGHCLNGRR.....PKSTVNDQNDQTKNDITG 195

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA Main:
- 1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
 - 4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 5: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1013	100.0	195	5	US-10-811-508-9
2	1007	99.4	195	5	US-10-722-045-52
3	950	93.8	194	5	US-10-722-045-51
4	950	93.8	194	5	US-10-672-302-19
5	819	80.8	186	5	US-10-722-045-53
6	383	37.8	176	5	US-10-672-302-20
7	381	37.6	176	5	US-10-722-045-54
8	376	37.1	186	5	US-10-722-045-50
9	369	36.4	184	5	US-10-868-381-34
10	369	36.4	184	5	US-10-722-045-48
11	358	35.3	186	5	US-10-722-045-49
12	357	35.2	187	4	US-10-371-264-42
13	357	35.2	187	4	US-10-371-099-338
14	357	35.2	187	4	US-10-371-122-338
15	357	35.2	187	4	US-10-373-567-42
16	357	35.2	187	4	US-10-628-088-338
17	357	35.2	187	5	US-10-831-780-338
18	357	35.2	187	5	US-10-722-045-47
19	357	35.2	187	5	US-10-466-811-94
20	357	35.2	187	5	US-10-831-781-42
21	356.5	35.2	187	4	US-10-371-264-45
22	356.5	35.2	187	4	US-10-371-099-341
23	356.5	35.2	187	4	US-10-371-122-341
24	356.5	35.2	187	4	US-10-373-567-45
25	356.5	35.2	187	4	US-10-628-088-341
26	356.5	35.2	187	5	US-10-831-780-341
27	356.5	35.2	187	5	US-10-831-781-45

Sequence 44, Appl
Sequence 340, App
Sequence 340, App
Sequence 44, Appl
Sequence 340, App
Sequence 340, App
Sequence 95, Appl
Sequence 100, App
Sequence 44, Appl
Sequence 43, Appl
Sequence 339, App
Sequence 339, App
Sequence 43, Appl
Sequence 339, App
Sequence 339, App
Sequence 4, Appl
Sequence 339, App
Sequence 43, Appl
Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-10-811-508-9
; Sequence 9, Application US/10811508
; Publication No. US20040224309A1
; GENERAL INFORMATION:
; APPLICANT: Medimmune Vaccines, Inc.
; APPLICANT: Cheng, Xing
; APPLICANT: Park, Hyun J
; APPLICANT: Jin, Hong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS INVOLVING RESPIRATORY SYNCYTIAL VIRUS SU
; TITLE OF INVENTION: STRAIN 9320
; FILE REFERENCE: 26-003820US/PC
; CURRENT APPLICATION NUMBER: US/10/811,508
; CURRENT FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; TYPE: PRT
; ORGANISM: respiratory syncytial virus B 9320
US-10-811-508-9

Query Match	100.0%;	Score 1013;	DB 5;	Length 195;
Best Local Similarity	100.0%;	Pred. No. 2.8e-88;	Mismatches 0;	Indels 0;
Matches 195;	Conservative 0;			Gaps 0;
Qy	1	MSRRNPCKFEIRGHCLNGRRCHYSHNYFEWPPHALLVRQNFMLNKLKSMDSIDTLSEI	60	
Db	1	MSRRNPCKFEIRGHCLNGRRCHYSHNYFEWPPHALLVRQNFMLNKLKSMDSIDTLSEI	60	
Qy	61	SGAAELDRTEYALGIVGVLESYIGSNINNTKQACVAMSKLLIENSDDIKKLRDNEEP	120	
Db	61	SGAAELDRTEYALGIVGVLESYIGSNINNTKQACVAMSKLLIENSDDIKKLRDNEEP	120	
Qy	121	NSPKIRVNTVVISYIESNRKNNKQTHLLKRLPADVLKTKTKNTLDIHKSTIISNPKEST	180	
Db	121	NSPKIRVNTVVISYIESNRKNNKQTHLLKRLPADVLKTKTKNTLDIHKSTIISNPKEST	180	
Qy	181	VNDQNDQTKNDITG	195	
Db	181	VNDQNDQTKNDITG	195	

RESULT 2

US-10-722-045-52
; Sequence 52, Application US/10722045
; Publication No. US20050053919A1
; GENERAL INFORMATION:
; APPLICANT: DeJong, Jan
; APPLICANT: Fouchier, Ronaldus

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OM protein - protein search, using sw model

Run on: December 27, 2005, 14:05:03 ; Search time 44.6875 Seconds
(without alignments)
360.767 Million cell updates/sec

Title: US-10-811-508-9
Perfect score: 1013
Sequence: 1 MSRRNPCKFEIRGHCLNGRR.....PKSTVNDQNDQTKNDITG 195

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfilese1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	809	79.9	186	4	PCT-US91-08177-15
2	179	17.7	30	2	US-09-511-023-2
3	176	17.4	30	2	US-09-511-023-8
4	175	17.3	30	2	US-09-511-023-4
5	173	17.1	30	2	US-09-511-023-5
6	172	17.0	30	2	US-09-511-023-7
7	171	16.9	30	2	US-09-511-023-6
8	170	16.8	30	2	US-09-511-023-10
9	169	16.7	30	2	US-09-511-023-3
10	169	16.7	30	2	US-09-511-023-9
11	110	10.9	2158	2	US-10-144-198-34
12	110	10.9	2158	2	US-10-144-198-35
13	110	10.9	2697	2	US-10-144-198-12
14	97.5	9.6	2189	2	US-10-172-502-2
15	97	9.6	709	2	US-09-248-796A-19045
16	93.5	9.2	565	2	US-09-248-796A-19208
17	93	9.2	257	1	US-07-781-355-2
18	92.5	9.1	1979	2	US-09-949-016-6468
19	92.5	9.1	2047	2	US-09-949-016-7404
20	92	9.1	635	2	US-09-248-796A-23137
21	89.5	8.8	463	2	US-09-979-275A-3
22	89.5	8.8	1279	2	US-09-710-279-3188
23	89.5	8.8	3696	2	US-09-134-001C-5080
24	88.5	8.7	360	1	US-08-317-223-2
25	88.5	8.7	360	1	US-08-445-135-3
26	88.5	8.7	360	2	US-09-059-849A-2
27	88.5	8.7	360	2	US-09-213-632-2

28	88.5	8.7	360	4	PCT-US95-12675-2	Sequence 2, Appli
29	88.5	8.7	404	2	US-09-248-796A-16463	Sequence 16463, A
30	88.5	8.7	461	1	US-08-630-822A-68	Sequence 68, Appl
31	88.5	8.7	461	1	US-09-005-069-68	Sequence 68, Appl
32	88.5	8.7	461	2	US-09-171-156A-27	Sequence 27, Appl
33	88.5	8.7	461	2	US-09-004-730A-27	Sequence 27, Appl
34	88.5	8.7	461	2	US-08-981-799A-27	Sequence 27, Appl
35	88.5	8.7	3712	2	US-10-037-417-48	Sequence 48, Appl
36	88.5	8.7	3712	2	US-10-037-417-51	Sequence 51, Appl
37	87	8.6	941	2	US-09-336-447A-9	Sequence 9, Appli
38	86.5	8.5	996	2	US-09-952-267B-9	Sequence 89, App
39	86.5	8.5	996	2	US-10-101-464A-889	Sequence 933, App
40	86.5	8.5	996	2	US-10-101-464A-933	Sequence 322, App
41	86.5	8.5	1087	2	US-09-830-230A-322	Sequence 321, App
42	86.5	8.5	1119	2	US-09-830-230A-321	Sequence 16, Appl
43	86.5	8.5	2110	2	US-09-809-665A-16	Sequence 2, Appli
44	86	8.5	984	1	US-08-242-932-2	Sequence 2, Appli
45	86	8.5	984	1	US-08-714-481-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
PCT-US91-08177-15
; Sequence 15, Application PC/TUS9108177
; GENERAL INFORMATION:
; APPLICANT: Samal, Siba K
; TITLE OF INVENTION: Bovine Respiratory Syncytial Virus Genes
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08177
; FILING DATE: 19911104
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/608,937
; FILING DATE: 05-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hightet, David W
; REGISTRATION NUMBER: 30,265
; REFERENCE/DOCKET NUMBER: 20509-96711
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-8300
; TELEFAX: 202-962-4854
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 186 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-08177-15

Query Match 79.9%; Score 809; DB 4; Length 186;
Best Local Similarity 80.1%; Pred. No. 2.3e-77;
Matches 149; Conservative 22; Mismatches 15; Indels 0; Gaps 0;
QY 1 MSRRNPCKFEIRGHCLNGRRCHYSHNYFEWPHALLVRQNFMLNKLKSMKSIDTLSEI 60
Db 1 MSRRNPCKFEIRGHCLNGRRCHYSHNYFEWPHALLVRQNFMLNKLKSMKSIDTLSEI 60
QY 61 SGAAELDRTEYALGVIGVLESYIGSINNITKQSAVCAMSKLLIIEINSDDIKKLRDNEP 120

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OM protein - protein search, using sw model

Run on: December 27, 2005, 14:09:54 ; Search time 9.47917 Seconds
(without alignments)
146.732 Million cell updates/sec

Title: US-10-811-508-9

Perfect score: 1013

Sequence: 1 MSRRNPKFIRGHCLNGRR.....PKSTVNDQDTKNDITG 195

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 54001 seqs, 7132810 residues

Total number of hits satisfying chosen parameters: 54001

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New.*

- 1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pap.*
- 2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pap.*
- 3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pap.*
- 4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pap.*
- 5: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pap.*
- 6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pap.*
- 7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pap.*
- 8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89.5	8.8	1279	6	US-10-793-626-3188
2	84.5	8.3	1126	6	US-10-485-517-248
3	81.5	8.0	1189	7	US-11-074-176-134
4	80	7.9	664	6	US-10-485-517-308
5	77.5	7.7	1032	6	US-10-392-234A-67
6	77	7.6	400	6	US-10-793-626-1056
7	77	7.6	989	6	US-10-821-234-975
8	76.5	7.6	273	6	US-10-793-626-608
9	76.5	7.6	282	6	US-10-353-783-56
10	76.5	7.6	416	6	US-10-793-626-2
11	76.5	7.6	5024	7	US-10-793-626-2964
12	75.5	7.5	454	7	US-11-089-551A-35
13	75	7.4	458	7	US-11-069-642-3
14	75	7.4	459	6	US-11-096-528-45
15	74	7.3	2333	7	US-11-096-281-13
16	74	7.3	2339	7	US-11-096-281-11
17	73.5	7.3	758	7	US-11-089-551A-31
18	73.5	7.3	3803	6	US-10-995-561-773
19	73.5	7.3	3960	6	US-10-995-561-771
20	73.5	7.3	5335	6	US-10-995-561-777
21	73.5	7.3	5406	6	US-10-995-561-774
22	73.5	7.3	5415	6	US-10-995-561-779
23	73.5	7.3	5464	6	US-10-995-561-775
24	73	7.2	708	7	US-11-196-475-76
25	73	7.2	1145	6	US-10-793-626-1432

26	72	7.1	170	6	US-10-689-742-16	Sequence 16, Appl
27	71	7.0	255	6	US-10-793-626-1304	Sequence 1304, Ap
28	71	7.0	348	6	US-10-793-626-1702	Sequence 1702, Ap
29	71	7.0	351	6	US-10-793-626-338	Sequence 338, App
30	71	7.0	540	6	US-10-821-234-1395	Sequence 1395, App
31	70.5	7.0	317	6	US-10-689-742-166	Sequence 166, App
32	70.5	7.0	1161	7	US-11-075-646-8	Sequence 8, Appl
33	70.5	7.0	1704	7	US-11-075-046-40	Sequence 40, Appl
34	70	6.9	700	7	US-11-196-475-66	Sequence 66, Appl
35	69.5	6.9	585	6	US-10-793-626-2124	Sequence 2124, Ap
36	69.5	6.9	792	7	US-11-088-686-29	Sequence 29, Appl
37	69	6.8	174	7	US-11-156-903-25	Sequence 25, Appl
38	69	6.8	451	6	US-10-793-626-210	Sequence 210, App
39	69	6.8	706	6	US-10-485-517-146	Sequence 146, App
40	69	6.8	794	6	US-10-485-517-355	Sequence 355, App
41	69	6.8	794	6	US-10-793-626-1050	Sequence 1050, Ap
42	69	6.8	1290	6	US-10-485-517-141	Sequence 141, App
43	68.5	6.8	149	7	US-11-156-903-27	Sequence 27, Appl
44	68.5	6.8	371	7	US-11-129-143-69	Sequence 69, Appl
45	68.5	6.8	379	6	US-10-510-386-76	Sequence 76, Appl

ALIGNMENTS

RESULT 1

US-10-793-626-3188
; Sequence 3188, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3188
; LENGTH: 1279
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-3188

Query Match	8.8%;	Score 89.5;	DB 6;	Length 1279;
Best Local Similarity	23.7%;	Pred. No. 2.8;		
Matches	40;	Conservative 26;	Mismatches 60;	Indels 43; Gaps 6;
QY	52 KSIDTLSEI-----	SGAAELDRTEYALGIVGVLESYIGSINNITKQSAVMSKLL	103	
DB	295 EADITITNIOANVAKKPSARVELDSKFE-----	DLKQINATPNATEEKKQDAIQRL-	346	
QY	104 IEINSDDIKCL-----	RNEEPNSPKIRVYNTVISYESNRKNKQTHLLKRLPADVLK	158	
DB	347 -NGKRDVKNLINQDRDNEVQHKHGLQLETHANPTKSD-----	ALQELQTKFIS	400	
QY	159 KT-----	IKNTLDIHSKITSINPKESTVNDQNDQTKNN	191	
DB	401 QTELINNNKDATNEEKDEAKRLLETSKNTITNIOAQTNQVNDNAKDN	449		

RESULT 2

US-10-485-517-248
; Sequence 248, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon

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OM protein - protein search, using sw model

Run on: December 27, 2005, 14:02:08 ; Search time 15.1771 Seconds
(without alignments)
589.584 Million cell updates/sec

Title: US-10-811-508-10
Perfect score: 499
Sequence: 1 MKMTKPKMILPDKYPCSI.....QFLQHLNIPEDITYTVILVS 93

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: piri:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	173	34.7	95	JQ1483	hypothetical 11-2K
2	73	14.6	314	E86482	protein F5J5.5 [im
3	73	14.6	373	T20723	hypothetical prote
4	70	14.0	391	T44839	probable amino-tra
5	69	13.8	185	B29324	hypothetical prote
6	69	13.8	233	JQ0296	CB81 protein precu
7	68.5	13.7	222	G64363	deoxyuridylate hyd
8	68.5	13.7	306	S41291	ornithine carbamoy
9	68.5	13.7	1164	T01871	RNA-directed DNA p
10	68	13.6	357	B90434	hypothetical prote
11	67	13.4	167	H90412	hypothetical prote
12	67	13.4	254	G64346	hypothetical prote
13	67	13.4	261	S04753	cytochrome-c oxida
14	66.5	13.3	322	T14597	proteinase homolog
15	66.5	13.3	324	T28331	ORF MSV170 hypote
16	66.5	13.3	482	T43996	virion protein [im
17	66.5	13.3	484	T44183	probable envelope
18	66	13.2	116	AE2400	hypothetical prote
19	66	13.2	489	AC2343	hypothetical prote
20	65.5	13.1	424	T04324	Gl/S transition co
21	65.5	13.1	476	G70175	aminoacyl-histidin
22	65.5	13.1	512	T09330	XIRP1 protein - hu
23	65.5	13.1	894	SYBYLM	leucine-tRNA ligas
24	65	13.0	439	H82875	oligopeptide trans
25	65	13.0	593	H64594	multidrug resistan
26	65	13.0	805	S13410	chloride channel p
27	65	13.0	810	S19725	voltage-gated chor
28	65	13.0	894	SYBYMX	leucine-tRNA ligas
29	65	13.0	2009	S49764	SEC7 protein - yea

30	64.5	12.9	785	2	T17309	probable ubiquitin
31	64.5	12.9	790	1	WMFM9	90K protein - alfa
32	64	12.8	169	2	T26882	hypothetical prote
33	64	12.8	285	2	A83104	protein C18B10.9 [
34	64	12.8	585	2	S48929	hypothetical prote
35	64	12.8	1242	2	T20739	hypothetical prote
36	63.5	12.7	233	2	S28226	nucleoside-diphosp
37	63.5	12.7	311	2	C70463	branched-chain ami
38	63.5	12.7	457	2	B97828	hypothetical prote
39	63.5	12.7	607	2	T11032	NADH2 dehydrogenas
40	63.5	12.7	716	2	D89837	hypothetical prote
41	63.5	12.7	981	2	T50851	receptor protein k
42	63.5	12.7	1009	2	C64483	hypothetical prote
43	63	12.6	415	2	AE2237	hypothetical prote
44	62.5	12.5	189	2	S48914	hypothetical prote
45	62.5	12.5	236	2	I64099	aerobic respiratio

ALIGNMENTS

RESULT 1

JQ1483
hypothetical 11.2K protein (M2-L intergenic region) - bovine respiratory syncytial virus
C:Species: bovine respiratory syncytial virus
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C:Accession: JQ1483

R:Zamora, M.; Samal, S.K.
J. Gen. Virol. 73, 737-741, 1992

A>Title: Sequence analysis of M2 mRNA of bovine respiratory syncytial virus obtained fr
A:Reference number: JQ1481, MUID:92185490; PMID:1312130
A:Accession: JQ1483

A:Molecule type: mRNA

A:Residues: 1-95 <ZAM>

A:Cross-references: UNIPROT:Q65704; UNIPARC:UPI00000F5BD2; GB:M82816; NID:g210823; PIDN

Query Match 34.7%; Score 173; DB 2; Length 95;
Best Local Similarity 38.9%; Pred. No. 3.7e-11;

Matches 37; Conservative 19; Mismatches 33; Indels 6; Gaps 2;

OY 1 MKMTKPKMILPDKYPCSISSILISSESMVATFNHNI---LQFNHNLHNQCILNHI 57

Db 3 MNKNMNSNIIIPPEKPCSISSLLIKENDVPVLSHQNVLDCLQFQYPNMYSQ---NHM 59

OY 58 FDEIHWTPKLLDTTQQLFQHLNIPEDITYTVILV 92

Db 60 LDDIYWTQSQELIEDVLKILHLSGINSKYIVYLV 94

RESULT 2

E86482

protein F5J5.5 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004

C:Accession: E86482

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141, MUID:21016719; PMID:11130712

A:Accession: E86482

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-314 <STO>

A:Cross-references: UNIPROT:Q9SKW5; UNIPARC:UPI000000C722; GB:AE005172; NID:g6598593;

C:Genetics:

A:Gene: F5J5.5

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OM protein - protein search, using sw model

Run on: December 27, 2005, 13:52:22 ; Search time 86.2188 Seconds
(without alignments)
473.937 Million cell updates/sec

Title: US-10-811-508-10
Perfect score: 499
Sequence: 1 MIKWTXPKIMLPDKYPCSI.....QFLQHLNIPEDIVTVYILVS 93

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	499	100.0	93	8 ADS91517	Adg91517 Human Res
2	295	59.1	90	8 ADO71204	Ado71204 Respirato
3	79	15.8	513	5 ABP28886	Abp28886 Streptoco
4	79	15.8	513	6 ABU46629	Abu46629 Protein e
5	74	14.8	314	7 ADD30320	Add30320 Plant yie
6	74	14.8	314	8 ADI44243	Adi44243 Plant tra
7	73	14.6	167	6 ADA34045	Ada34045 Acinetoba
8	73	14.6	301	8 ADI44137	Adi44137 Plant tra
9	73	14.6	301	8 ADO61745	Ado61745 Transcrip
10	73	14.6	314	7 ADD30262	Add30262 Plant yie
11	73	14.6	373	8 ADN22554	Adn22554 Bacterial
12	70	14.0	420	7 ABM88301	Abm88301 Rice abio
13	70	14.0	428	5 ABP73645	Abp73645 Candida a
14	70	14.0	2225	4 ABB71877	Abb71877 Drosophil
15	69	13.8	386	9 AEB41199	Aeb41199 L. pneumo
16	69	13.8	388	9 AEB37894	Aeb37894 L. pneumo
17	68.5	13.7	261	6 ABM70801	Abm70801 Staphyloc
18	68.5	13.7	305	8 ADS25036	Ads25036 Bacterial
19	68.5	13.7	347	5 ABB84769	Abb84769 DNA polym
20	68.5	13.7	2138	5 AAE52955	Aae52955 Human nuc
21	67.5	13.5	248	8 ADX93110	Adx93110 Plant ful
22	67	13.4	166	4 AAG82165	Ag82165 S. epider
23	67	13.4	166	4 AAG82847	Ag82847 S. epider
24	67	13.4	219	8 ADZ74039	Adz74039 Staphyloc

25	67	13.4	222	5 ABP38367	Abp38367 Staphyloc
26	67	13.4	386	6 ABM68982	Abm68982 Phototrab
27	66.5	13.3	353	6 ADA33943	Ada33943 Acinetoba
28	66	13.2	50	4 AAM87388	Aam87388 Human imm
29	66	13.2	211	6 ADB07636	Adb07636 Alloioococ
30	66	13.2	248	6 ADB07638	Adb07638 Alloioococ
31	66	13.2	499	7 ADF06240	Adf06240 Bacterial
32	65.5	13.1	83	3 AAG23566	Aag23566 Arabidops
33	65.5	13.1	83	3 AAG05347	Aag05347 Arabidops
34	65	13.0	740	5 ABP73836	Abp73836 Candida a
35	65	13.0	2000	6 ABR52951	Ab52951 Protein e
36	65	13.0	2000	7 ADK62374	Adk62374 Disease t
37	64.5	12.9	218	4 AAB63744	Aab63744 Human pro
38	64.5	12.9	232	3 AAG52539	Aag52539 Arabidops
39	64.5	12.9	232	3 AAG36804	Aag36804 Arabidops
40	64.5	12.9	232	3 AAG07479	Aag07479 Arabidops
41	64.5	12.9	245	3 AAG36803	Aag36803 Arabidops
42	64.5	12.9	245	3 AAG52538	Aag52538 Arabidops
43	64.5	12.9	245	3 AAG07478	Aag07478 Arabidops
44	64.5	12.9	317	3 AAG07477	Aag07477 Arabidops
45	64.5	12.9	317	3 AAG36802	Aag36802 Arabidops

ALIGNMENTS

RESULT 1
ADS91517
ID ADS91517 standard; protein; 93 AA.
XX ADS91517;
AC ADS91517;
DT 30-DEC-2004 (first entry)
XX Human Respiratory syncytial virus (RSV) 9320 protein - SEQ ID 10.
DE Human Respiratory syncytial virus (RSV) 9320 protein - SEQ ID 10.
XX Respiratory syncytial virus genome; vaccine;
KW Respiratory syncytial virus genome; vaccine;
KW viral respiratory tract disease; pneumonia; bronchiolitis.
XX Human Respiratory syncytial virus 9320.
OS Human Respiratory syncytial virus 9320.
XX WO2004087062-A2.
PN WO2004087062-A2.
PD 14-OCT-2004.
XX 14-OCT-2004.
PF 26-MAR-2004; 2004WO-US009438.
XX 26-MAR-2004; 2003US-0458331P.
PR 28-MAR-2003; 2003US-0458331P.
PR 03-OCT-2003; 2003US-0508320P.
XX (MEDI-) MEDIMUNE VACCINES INC.
XX Cheng X, Park HJ, Jin H;
XX WPI; 2004-737511/72.
DR N-PSDB; ADS91508.
XX New recombinant nucleic acid of the human respiratory syncytial virus
PT subgroup B strain 9320 genome, useful in preparing a vaccine composition
PT against respiratory syncytial virus.
XX Claim 46; SEQ ID NO 10; 137pp; English.
XX The invention comprises an antigenomic cDNA sequence from Human
CC Respiratory syncytial virus (RSV) 9320. The invention also comprises
CC amino acid sequences encoded by the RSV 9320 cDNA sequence of the
CC invention. The DNA and protein sequences of the invention are useful as
CC vaccine against Human RSV and therefore useful for the prevention of
CC viral respiratory tract disease (e.g. bronchiolitis and pneumonia). The
CC present amino acid sequence represents a Human RSV 9320 protein of the
XX invention.
XX Sequence 93 AA;

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OM protein - protein search, using sw model

Run on: December 27, 2005, 14:05:13 ; Search time 71.3646 Seconds
(without alignments)
544.502 Million cell updates/sec

Title: US-10-811-508-10
Perfect score: 499
Sequence: 1 MIKMTKPKMILDPKPCSI.....QFLQHLNIPEDIVTVYILVS 93

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:
1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp:
2: /cgm2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp:
3: /cgm2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp:
4: /cgm2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp:
5: /cgm2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp:
6: /cgm2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	499	100.0	93	5	US-10-811-508-10
2	459	92.0	90	5	US-10-722-045-60
3	303	60.7	90	5	US-10-722-045-59
4	295	59.1	90	5	US-10-672-302-84
5	168	33.7	90	5	US-10-722-045-61
6	88.5	17.7	2110	5	US-10-732-923-8666
7	79.5	15.9	123	4	US-10-425-115-321017
8	79	15.8	513	4	US-10-282-122A-74553
9	78.5	15.7	117	4	US-10-437-963-119754
10	74	14.8	314	4	US-10-225-066A-352
11	74	14.8	314	4	US-10-374-780A-2706
12	74	14.8	314	5	US-10-225-066A-352
13	73.5	14.7	380	5	US-10-732-923-19424
14	73	14.6	301	4	US-10-374-780A-2600
15	73	14.6	314	4	US-10-225-066A-294
16	73	14.6	314	5	US-10-732-923-5335
17	73	14.6	314	5	US-10-225-066A-294
18	73	14.6	373	4	US-10-369-493-5207
19	72	14.4	374	5	US-10-732-923-19416
20	71.5	14.3	123	5	US-10-732-923-3725
21	70	14.0	335	4	US-10-424-599-147263
22	70	14.0	428	4	US-10-032-585-7482
23	70	14.0	2225	6	US-11-097-143-42423
24	68.5	13.7	305	4	US-10-369-493-14069
25	68.5	13.7	347	3	US-09-906-179A-138
26	68.5	13.7	1327	4	US-10-425-115-215557
27	68.5	13.7	1370	4	US-10-425-115-215790

28	68	13.6	82	4	US-10-437-963-139718	Sequence 139718,
29	68	13.6	360	4	US-10-437-963-169721	Sequence 169721,
30	67.5	13.5	248	4	US-10-425-114-55774	Sequence 55774, A
31	67.5	13.5	309	4	US-10-425-115-315982	Sequence 315982,
32	67	13.4	220	4	US-10-424-599-183874	Sequence 183874,
33	66.5	13.3	1087	4	US-10-425-115-215821	Sequence 215821,
34	66	13.2	211	5	US-10-501-282-1576	Sequence 1576, Ap
35	66	13.2	248	5	US-10-501-282-1578	Sequence 1578, Ap
36	65.5	13.1	370	4	US-10-437-963-149586	Sequence 149586,
37	65	13.0	200	5	US-10-732-923-15810	Sequence 15810, A
38	65	13.0	263	4	US-10-424-599-229207	Sequence 229207,
39	65	13.0	403	4	US-10-425-115-251702	Sequence 251702,
40	65	13.0	740	4	US-10-032-585-7673	Sequence 7673, Ap
41	64.5	12.9	546	4	US-10-014-162-109	Sequence 109, App
42	64.5	12.9	661	4	US-10-437-963-183011	Sequence 183011,
43	64.5	12.9	785	4	US-10-408-765A-357	Sequence 357, App
44	64	12.8	432	4	US-10-424-599-209041	Sequence 209041,
45	64	12.8	668	4	US-10-424-599-278303	Sequence 278303,

ALIGNMENTS

RESULT 1

US-10-811-508-10
; Sequence 10, Application US/10811508
; Publication No. US20040224309A1
; GENERAL INFORMATION:
; APPLICANT: Medimmune Vaccines, Inc.
; APPLICANT: Cheng, Xing
; APPLICANT: Park, Hyun J
; APPLICANT: Jin, Hong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS INVOLVING RESPIRATORY SYNCYTIAL VIRUS SU
; TITLE OF INVENTION: STRAIN 9320
; FILE REFERENCE: 26-003820US/PC
; CURRENT FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; TYPE: PRT
; ORGANISM: respiratory syncytial virus B 9320
US-10-811-508-10

Query Match	100.0%;	Score	499;	DB	5;	Length	93;
Best local similarity	100.0%;	Pred. No.	1.9e-50;				
Matches	93;	Conservative	0;	Mismatches	0;	Indels	0;
Qy	1	MIKMTKPKMILDPKPCSISSILISSESVATFNHKNILQFNHNLHLDNHQCLLNHIHIDE	60				
Db	1	MIKMTKPKMILDPKPCSISSILISSESVATFNHKNILQFNHNLHLDNHQCLLNHIHIDE	60				
Qy	61	IHWTPKNLLDTTQOFLQHLNIPEDIVTVYILVS	93				
Db	61	IHWTPKNLLDTTQOFLQHLNIPEDIVTVYILVS	93				

RESULT 2

US-10-722-045-60
; Sequence 60, Application US/10722045
; Publication No. US20050053919A1
; GENERAL INFORMATION:
; APPLICANT: DeJong, Jan
; APPLICANT: Fouchier, Ronaldus
; APPLICANT: Van Den Hoogen, Bernadetta
; APPLICANT: Osterhaus, Albertus
; APPLICANT: Groen, Jan
; TITLE OF INVENTION: Virus causing respiratory tract illness in susceptible mammals
; FILE REFERENCE: 7862-108-999
; CURRENT APPLICATION NUMBER: US/10/722,045
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 10/466,811

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OM protein - protein search, using sw model

Run on: December 27, 2005, 13:52:22 ; Search time 180.781 Seconds
(without alignments)
473.937 Million cell updates/sec

Title: US-10-811-508-9
Perfect score: 1013
Sequence: 1 MSRRNPCKFEIRGHCLNGRR.....PKSTVNDQNDQTKNDITG 195

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1013	100.0	195	8 ADS91516	ADS91516 Human Res
2	950	93.8	194	1 AAP70785	Aap70785 Sequence
3	950	93.8	194	1 AAP70477	Aap70477 Sequence
4	950	93.8	194	2 AAW47606	Aaw47606 HRSV prot
5	950	93.8	194	8 ADO71171	Ado71171 Respirato
6	940	92.8	194	2 AAR25303	Aar25303 HRSV 22K
7	801	79.1	186	2 AAR24190	Aar24190 Bovine RS
8	383	37.8	176	8 ADO71172	Ado71172 Pneumonia
9	369	36.4	184	8 ADO30912	Adg30912 Avian pne
10	357	35.2	187	5 AAG97869	Abg97869 Negative-
11	357	35.2	187	5 AAG97857	Abg97857 Negative-
12	357	35.2	187	7 ADF68667	Adf68667 Human met
13	357	35.2	187	7 ADF89240	Adf89240 M2-1 prot
14	357	35.2	187	8 ADJ97128	Adj97128 M2-1 prot
15	357	35.2	187	8 ADL07779	Adl07779 M2-1 prot
16	357	35.2	187	8 ADM67599	Adm67599 Human met
17	357	35.2	187	8 ADU26100	Adu26100 Human met
18	357	35.2	187	9 ADY84172	Ady84172 M2-1 prot
19	356.5	35.2	187	7 ADF68670	Adf68670 Human met
20	356.5	35.2	187	7 ADF89243	Adf89243 M2-1 prot
21	356.5	35.2	187	8 ADJ97131	Adj97131 M2-1 prot
22	356.5	35.2	187	8 ADL07782	Adl07782 M2-1 prot
23	356.5	35.2	187	8 ADM67602	Adm67602 Human met
24	356.5	35.2	187	8 ADU26103	Adu26103 Human met

25	356.5	35.2	187	9 ADY84175	Ady84175 M2-1 prot
26	352.5	34.8	187	5 AEG97870	Abg97870 Negative-
27	352.5	34.8	187	7 ADF68669	Adf68669 Human met
28	352.5	34.8	187	7 ADF89242	Adf89242 M2-1 prot
29	352.5	34.8	187	8 ADJ97130	Adj97130 M2-1 prot
30	352.5	34.8	187	8 ADL07781	Adl07781 M2-1 prot
31	352.5	34.8	187	8 ADM67601	Adm67601 Human met
32	352.5	34.8	187	8 ADU26102	Adu26102 Human met
33	352.5	34.8	187	9 ADY84174	Ady84174 M2-1 prot
34	351	34.6	187	7 ADF68668	Adf68668 Human met
35	351	34.6	187	7 ADF89241	Adf89241 M2-1 prot
36	351	34.6	187	8 ADJ97129	Adj97129 M2-1 prot
37	351	34.6	187	8 ADL07780	Adl07780 M2-1 prot
38	351	34.6	187	8 ADM67600	Adm67600 Human met
39	351	34.6	187	8 ADU26101	Adu26101 Human met
40	351	34.6	187	9 ADV68224	Adv68224 HMPV (str
41	351	34.6	187	9 ADY84173	Ady84173 M2-1 prot
42	179	17.7	30	3 AAB08798	Aab08798 Amino aci
43	179	17.7	30	8 ADO71173	Ado71173 Respirato
44	176	17.4	30	3 AAB08804	Aab08804 Amino aci
45	175	17.3	30	3 AAB08800	Aab08800 Amino aci

ALIGNMENTS

RESULT 1
ADS91516
ID ADS91516 standard; protein; 195 AA.
AC ADS91516;
XX
XX
DT 30-DEC-2004 (first entry)
XX
DS Human Respiratory syncytial virus (RSV) 9320 protein - SEQ ID 9.
XX
KW Respiratory syncytial virus genome; vaccine;
KW viral respiratory tract disease; pneumonia; bronchiolitis.
XX
OS Human Respiratory syncytial virus 9320.
XX
PN WO2004087062-A2.
XX
PD 14-OCT-2004.
XX
PF 26-MAR-2004; 2004WO-US009438.
XX
PR 28-MAR-2003; 2003US-0458331P.
PR 03-OCT-2003; 2003US-0508320P.
XX
XX (MEDI-) MEDIMMUNE VACCINES INC.
XX
XX Cheng X, Park HJ, Jin H;
XX WPI; 2004-737511/72.
XX N-PSDB; ADS91508.
XX
XX New recombinant nucleic acid of the human respiratory syncytial virus subgroup B strain 9320 genome, useful in preparing a vaccine composition against respiratory syncytial virus.
XX
XX Claim 46; SEQ ID NO 9; 137pp; English.
XX
XX The invention comprises an antigenomic cDNA sequence from Human Respiratory syncytial virus (RSV) 9320. The invention also comprises amino acid sequences encoded by the RSV 9320 cDNA sequence of the invention. The DNA and protein sequences of the invention are useful as vaccine against Human RSV and therefore useful for the prevention of viral respiratory tract disease (e.g. bronchiolitis and pneumonia). The present amino acid sequence represents a Human RSV 9320 protein of the invention.

Sequence 195 AA;

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OM protein - protein search, using sw model

Run on: December 27, 2005, 14:02:08 ; Search time 31.8229 Seconds
(without alignments)
589.584 Million cell updates/sec

Title: US-10-811-508-9
Perfect score: 1013
Sequence: 1 MSRRNPCKFEIRGHCLNGRR.....PKSTVNDQDQTKNDITG 195

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	950	93.8	194	1 WMNZ22	envelope-associate
2	809	79.9	186	1 WMNZBA	matrix glycoprotei
3	376	37.1	186	1 JQ1623	envelope-associate
4	376	37.1	186	2 JQ1987	hypothetical 21.0K
5	103.5	10.2	986	2 E90596	restriction-modifi
6	103.5	10.2	986	2 S49394	HsdR1 protein - My
7	103.5	10.2	986	2 H90565	restriction modifi
8	99.5	9.8	609	2 S46019	YswI protein - yea
9	99	9.8	628	2 A82889	hypothetical prote
10	99	9.8	1864	2 T18485	hypothetical prote
11	97.5	9.6	201	2 S05436	dnak-type molecula
12	96.5	9.5	912	2 H90567	hypothetical prote
13	96	9.5	597	2 F82935	DNA polymerase III
14	96	9.5	807	2 B71605	hypothetical prote
15	95	9.4	5005	2 F82884	hypothetical prote
16	94.5	9.3	504	2 S33193	phase-1 flagellin
17	94.5	9.3	504	2 S33190	phase-1 flagellin
18	94.5	9.3	504	2 S33191	phase-1 flagellin
19	94.5	9.3	504	2 S33194	phase-1 flagellin
20	94.5	9.3	504	2 S33186	phase-1 flagellin
21	94.5	9.3	504	2 S33189	phase-1 flagellin
22	94.5	9.3	504	2 S33188	phase-1 flagellin
23	94.5	9.3	504	2 S33187	phase-1 flagellin
24	94.5	9.3	507	2 S33185	phase-1 flagellin
25	94.5	9.3	507	2 S33192	phase-1 flagellin
26	94.5	9.3	508	2 A53465	phase 1 flagellin
27	94	9.3	2269	2 T28677	rhoptry protein -
28	93.5	9.2	598	2 D81420	hypothetical prote
29	93.5	9.2	761	2 T03719	probable thyroid r

30	93.5	9.2	2186	2 H89960	hypothetical prote
31	93.5	9.2	2485	1 H71621	serine/threonine-s
32	93.5	9.2	3191	2 T22945	hypothetical prote
33	93.5	9.2	6713	2 B89921	hypothetical prote
34	93	9.2	257	2 B70246	outer surface prot
35	92.5	9.1	1941	2 T30554	ubiquitin-protein
36	92	9.1	1166	2 H71609	hypothetical prote
37	92	9.1	1256	2 S14556	asparagine-rich pr
38	91.5	9.0	342	2 G64411	hypothetical prote
39	91	9.0	1252	2 B42771	reticulocyte-bind
40	90.5	8.9	644	2 T47835	hypothetical prote
41	89.5	8.8	463	2 JC7372	toxan-A - jellyfis
42	89.5	8.8	504	2 T10558	hypothetical prote
43	89	8.8	2401	2 T28676	rhoptry protein -
44	89	8.8	3724	2 T18427	hypothetical prote
45	88.5	8.7	696	2 G71620	hypothetical prote

ALIGNMENTS

RESULT 1

WMNZ22

envelope-associated 22K protein - human respiratory syncytial virus

C:Species: human respiratory syncytial virus

C>Date: 30-Jun-1987 #sequence revision 30-Jun-1987 #text_change 09-Jul-2004

C:Accession: B93010; A93009; A04034

R:Elango, N.; Satake, M.; Venkatesan, S.

J. Virol. 55, 101-110, 1985

A>Title: mRNA sequence of three respiratory syncytial virus genes encoding two nonstruc

A:Reference number: A93010; MUID:85237684; PMID:4009789

A:Accession: B93010

A:Molecule type: genomic RNA

A:Residues: 1-194 <ELA>

A:Cross-references: UNIPROT:P04545; UNIPARC:UPI0000000135; GB:M11486; NID:G333925; PIDN

R:Collins, P.L.; Wertz, G.W.

J. Virol. 54, 65-71, 1985

A>Title: The envelope-associated 22K protein of human respiratory syncytial virus: nucl.

A:Reference number: A93009; MUID:85135082; PMID:3838351

A:Accession: A93009

A:Molecule type: genomic RNA

A:Residues: 1-194 <COL>

A:Cross-references: UNIPARC:UPI0000000135; GB:M11486; GB:K01459; GB:K02719; GB:K03348;

D:G333925; PIDN:AAB59860.1; PID:G333934

C:Genetics:

A:Gene: 22K

C:Superfamily: respiratory syncytial virus envelope-associated 22K protein

C:Keywords: glycoprotein

F:89,191/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 93.8%; Score 950; DB 1; Length 194;
Best Local Similarity 93.3%; Pred. No. 2.2e-65; Mismatches 6; Indels 0; Gaps 0;
Matches 181; Conservative 7;

QY 1 MSRRNPCKFEIRGHCLNGRRCHYSHNYFEWPPHALLVRQNFMLNKLKSMKSIDTLSEI 60

Db 1 MSRRNPCKFEIRGHCLNGRRCHYSHNYFEWPPHALLVRQNFMLNKLKSMKSIDTLSEI 60

QY 61 SGAELDRTEYALGIVGVLSYIGSINNITKQSAVCVMSKLLIENSDDIKKLDRNEBP 120

Db 61 SGAELDRTEYALGIVGVLSYIGSINNITKQSAVCVMSKLLIENSDDIKKLDRNEBP 120

QY 121 NSPKIRVNTVTSYTESNRKNNKQTHLLKRLPADVLKKTIKNTLDIHKSITINPKEST 180

Db 121 NSPKIRVNTVTSYTESNRKNNKQTHLLKRLPADVLKKTIKNTLDIHKSITINPKEST 180

QY 181 VNDQNDQTKNDIT 194

Db 181 VSDTNDHAKNDIT 194

RESULT 2

WMNZBA

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 27, 2005, 14:09:54 ; Search time 4.52083 Seconds
(without alignments)
146.732 Million cell updates/sec

Title: US-10-811-508-10

Perfect score: 499

Sequence: 1 MIMWTKMILPKYPCSI.....QFLOHNLNIPEDITYTVILVS 93

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 54001 seqs, 7132810 residues

Total number of hits satisfying chosen parameters: 54001

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_New.*

- 1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pap.*
- 2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pap.*
- 3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pap.*
- 4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pap.*
- 5: /cgn2_6/prodata/2/pubpaa/US05_NEW_PUB.pap.*
- 6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pap.*
- 7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pap.*
- 8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	13.4	166	6	US-10-793-626-1424
2	67	13.4	166	6	US-10-793-626-2788
3	61	12.2	409	7	US-11-102-240-22
4	59	11.8	687	6	US-10-821-234-1197
5	58.5	11.7	258	6	US-10-793-626-666
6	58	11.6	1145	6	US-10-793-626-1424
7	57.5	11.5	431	6	US-10-467-657-1322
8	57.5	11.5	471	6	US-10-467-962B-10
9	56.5	11.3	311	6	US-10-793-626-2460
10	56	11.2	300	6	US-10-667-295-117
11	56	11.2	302	6	US-10-667-295-116
12	56	11.2	316	6	US-10-667-295-115
13	55.5	11.1	305	6	US-10-793-626-1264
14	55	11.0	447	7	US-11-112-882-20
15	55	11.0	470	6	US-10-873-528-3
16	54.5	10.9	453	6	US-10-466-794A-5
17	54	10.8	752	6	US-10-793-626-348
18	54	10.8	858	6	US-10-395-561-874
19	54	10.8	858	6	US-10-395-561-875
20	53.5	10.7	808	7	US-11-110-082-38
21	53	10.6	612	7	US-11-186-284-136
22	53	10.6	620	7	US-11-186-284-134
23	53	10.6	621	6	US-10-821-234-1376
24	53	10.6	622	7	US-11-021-441-35
25	53	10.6	916	6	US-10-467-657-4242

26	53	10.6	970	6	US-10-770-726-86	Sequence 86, Appl
27	52.5	10.5	754	6	US-10-793-626-1296	Sequence 1296, Ap
28	52	10.4	102	6	US-10-928-446A-146	Sequence 146, App
29	52	10.4	178	6	US-10-667-295-131	Sequence 131, App
30	52	10.4	184	6	US-10-667-295-130	Sequence 130, App
31	52	10.4	272	6	US-10-873-528-71	Sequence 71, Appl
32	52	10.4	315	6	US-10-793-626-2100	Sequence 2100, Ap
33	52	10.4	383	6	US-10-793-626-1564	Sequence 1564, App
34	52	10.4	392	7	US-11-084-458-2	Sequence 2, Appli
35	52	10.4	465	6	US-10-793-626-1676	Sequence 1676, Ap
36	52	10.4	928	6	US-10-841-129-4	Sequence 4, Appli
37	51.5	10.3	106	7	US-11-000-463-777	Sequence 777, App
38	51.5	10.3	226	6	US-10-793-626-1734	Sequence 1734, Ap
39	51.5	10.3	303	6	US-10-467-657-6810	Sequence 6810, Ap
40	51.5	10.3	357	7	US-11-129-143-73	Sequence 73, Appl
41	51.5	10.3	412	6	US-10-858-730-82	Sequence 82, Appl
42	51.5	10.3	574	6	US-10-518-341-1	Sequence 1, Appli
43	51.5	10.3	574	7	US-11-022-562-214	Sequence 214, App
44	51.5	10.3	781	7	US-11-194-246-344	Sequence 344, App
45	51.5	10.3	965	7	US-11-172-145-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-793-626-1424
; Sequence 1424, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1424
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1424

Query Match 13.4%; Score 67; DB 6; Length 166;
Best Local Similarity 23.9%; Pred. No. 0.77;
Matches 22; Conservative 19; Mismatches 35; Indels 16; Gaps 3;

QY 13 PKYPCSTSSILISSESVAFTN-HK-----NLFQFNHLDHQCILNIPDE 60
DB 67 PDKQVLDINGIITIDKAFKVTNGHQLTKTTEYDLYVLAERNHVMQREILDHVMGY 126
QY 61 IHWTPKNDLTTQOFLQH---LNIPEDITYV 88
DB 127 NSEVTNVVDVYIRYLRNKLKPFNKESITV 158

RESULT 2
US-10-793-626-2788
; Sequence 2788, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09

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OM protein - protein search, using sw model

Run on: December 27, 2005, 14:05:03 ; Search time 21.3125 seconds
(without alignments)
360.767 Million cell updates/sec

Title: US-10-811-508-10
Perfect score: 499
Sequence: 1 MTKYKPKMILDKYPCSI.....QFLQHLNIPEDITYVILVS 93

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/aaa/5 COMB.pcp.*
2: /cgn2_6/prodata/1/aaa/6 COMB.pcp.*
3: /cgn2_6/prodata/1/aaa/H COMB.pcp.*
4: /cgn2_6/prodata/1/aaa/PCTUS COMB.pcp.*
5: /cgn2_6/prodata/1/aaa/RE COMB.pcp.*
6: /cgn2_6/prodata/1/aaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	14.6	167	2	US-09-328-352-5332
2	70.5	14.1	433	2	US-09-248-796A-24548
3	70	14.0	110	2	US-09-270-767-32810
4	70	14.0	110	2	US-09-270-767-48027
5	68.5	13.7	441	2	US-09-248-796A-26086
6	67	13.4	166	2	US-09-710-279-1424
7	67	13.4	166	2	US-09-710-279-1424
8	67	13.4	222	2	US-09-134-001C-3212
9	66.5	13.3	353	2	US-09-248-796A-25703
10	66	13.2	499	2	US-09-543-681A-5525
11	66	13.2	499	2	US-09-543-681A-5525
12	65.5	13.1	70	2	US-09-248-796A-25792
13	65	13.0	743	2	US-09-248-796A-25792
14	64.5	12.9	186	2	US-09-270-767-37935
15	64.5	12.9	186	2	US-09-270-767-37935
16	64.5	12.9	438	2	US-09-248-796A-23919
17	64.5	12.9	806	2	US-09-949-016-7572
18	64	12.8	121	1	US-08-450-257-55
19	64	12.8	121	1	US-08-450-246-55
20	64	12.8	121	1	US-08-450-098-55
21	64	12.8	121	1	US-08-451-233-55
22	64	12.8	121	1	US-08-450-236-55
23	64	12.8	121	2	US-08-235-403-55
24	63.5	12.7	306	2	US-09-724-623-110
25	63.5	12.7	317	2	US-09-134-000C-5888
26	63.5	12.7	322	2	US-09-248-796A-24574
27	63.5	12.7	435	4	PCT-US94-01321-12

28	63	12.6	256	2	US-09-107-532A-4083	Sequence 4083, Ap
29	63	12.6	287	1	US-08-365-981-9	Sequence 9, Appli
30	63	12.6	383	2	US-09-248-796A-20241	Sequence 20241, A
31	63	12.6	593	2	US-09-543-681A-5368	Sequence 5368, Ap
32	62.5	12.5	123	1	US-08-094-128A-25	Sequence 25, Appl
33	62.5	12.5	123	1	US-08-455-674-25	Sequence 25, Appl
34	62.5	12.5	123	1	US-08-455-992-25	Sequence 25, Appl
35	62.5	12.5	123	1	US-08-455-972-25	Sequence 25, Appl
36	62.5	12.5	123	4	PCT-US92-00652-25	Sequence 25, Appl
37	62.5	12.5	345	2	US-09-540-236-2938	Sequence 2938, Ap
38	62.5	12.5	1015	2	US-09-283-385C-2	Sequence 2, Appli
39	62.5	12.5	2954	2	US-09-150-867-1	Sequence 1, Appli
40	62	12.4	157	2	US-09-134-001C-3827	Sequence 3827, Ap
41	62	12.4	249	2	US-09-543-681A-5381	Sequence 5381, Ap
42	61.5	12.3	213	2	US-09-107-532A-5566	Sequence 5566, Ap
43	61.5	12.3	362	2	US-08-637-670-35	Sequence 35, Appl
44	61.5	12.3	807	2	US-09-538-092-574	Sequence 574, App
45	61	12.2	121	1	US-08-450-257-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1

US-09-328-352-5332
; Sequence 5332, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5332
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5332

Query Match	14.6%	Score 73;	DB 2;	Length 167;
Best Local Similarity	33.3%	Pred. No. 0.21;		
Matches	29;	Conservative	13;	Mismatches 33;
			Indels	12;
			Gaps	5;
Qy	8	KIMILPKYPCSISSILISSE-----SVVTFNHNILQFNHNH-----LDNHQCLLNHIF	58	
Db	12	KLKVKATSKFPGKIRSLTMSKAFGRIVPMVGTANIR-YLEVNVNHTVLENGKQNMQNH1-	69	
Qy	59	DEIHWTPKNLL-DTTQOPLQHLNIPED	84	
Db	70	KGVAAMALLAETATGTLGLHIPDN	96	

RESULT 2

US-09-248-796A-24548
; Sequence 24548, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24548
; LENGTH: 433
; TYPE: PRT

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OM protein - protein search, using sw model

Run on: December 27, 2005, 14:01:48 ; Search time 199.74 Seconds
(without alignments)
688.787 Million cell updates/sec

Title: US-10-811-508-9
Perfect score: 1013
Sequence: 1 MSRRNPCKFEIRGCHLNGRR.....PKSTVNDQDQTKNNDITG 195

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	1013	100.0	195	2	Q6V2E6_HRSV
2	1007	99.4	195	2	O42050_HRSV
3	952	94.0	194	2	Q76TK9_9MONO
4	952	94.0	194	2	Q84196_HRSV
5	950	93.8	194	1	VMA2_HRSVA
6	950	93.8	194	2	Q771A8_HRSV
7	944	93.2	194	2	Q4KRW3_HRSV
8	830	81.9	186	1	VMA2_ORSVV
9	819	80.8	186	2	Q77KZ7_BRSVA
10	819	80.8	186	2	Q9YS23_9MONO
11	809	79.9	186	1	VMA2_BRSVA
12	809	79.9	186	2	Q77K19_BRSVA
13	383	37.8	176	2	Q5MKW8_9MONO
14	383	37.8	176	2	Q50EW4_9MONO
15	383	37.8	176	2	Q5MKM1_MPV15
16	376	37.1	186	1	VMA2_TRTV
17	376	37.1	186	2	Q5USAO_9MONO
18	374	36.9	184	2	Q91R59_9MONO
19	373	36.8	184	2	Q91011_9MONO
20	373	36.8	184	2	Q91R55_9MONO
21	373	36.8	184	2	Q91CC8_9MONO
22	372	36.7	184	2	Q91R62_9MONO
23	371	36.6	184	2	Q91R57_9MONO
24	369	36.4	184	2	Q9QF46_9MONO
25	367	36.2	184	2	Q91R54_9MONO
26	367	36.2	184	2	Q91R56_9MONO
27	364	35.9	186	2	Q8JUT6_TRTV
28	364	35.9	184	2	Q91R60_9MONO
29	359	35.4	187	2	Q6QQH2_9MONO
30	358	35.3	186	2	Q91SF9_9MONO
31	357	35.2	187	2	Q8QN58_9MONO

32	356	35.1	187	2	Q6QQG4_9MONO	Q6qg94 human metap
33	355.5	35.1	187	2	Q6WBA6_9MONO	Q6wba6 human metap
34	354	34.9	187	2	Q6QQI6_9MONO	Q6qqi6 human metap
35	352.5	34.8	192	2	Q6E7G0_9MONO	Q6e7g0 human metap
36	351.5	34.7	187	2	Q6QQF6_9MONO	Q6qqf6 human metap
37	351	34.6	187	2	Q6WB97_9MONO	Q6wb97 human metap
38	348	34.4	187	2	Q6QQE8_9MONO	Q6qqe8 human metap
39	347	34.3	184	2	Q91R61_9MONO	Q91r61 avian pneum
40	342	33.8	184	2	Q91R58_9MONO	Q91r58 avian pneum
41	120.5	11.9	735	2	Q421W3_PLABE	Q421w3 plasmodium
42	117.5	11.6	1740	2	Q81JK9_PLAF7	Q81jk9 plasmodium
43	117.5	11.6	7170	2	Q81L30_PLAF7	Q81l30 plasmodium
44	114	11.3	2798	1	NPBL_MOUSE	Q6kcd5 mus musculus
45	112	11.1	846	2	Q4Y612_PLACH	Q4y612 plasmodium

ALIGNMENTS

RESULT 1

Q6V2E6_HRSV
ID Q6V2E6_HRSV PRELIMINARY; PRT; 195 AA.
AC Q6V2E6_...
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE M2-1.
OS Human Respiratory syncytial virus 9320.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=253182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cheng X., Park H., Jin H.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY353550; AAR14267.1; -; Genomic RNA.
DR GO; GO:0039031; C:Viral envelope; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0046782; P:regulation of viral transcription; IEA.
DR InterPro; IPR009452; Pneumovirus_M2.
DR InterPro; IPR000571; Znf_CCH.
DR Pfam; PF06436; Pneumovirus_M2; 1.
DR Pfam; PF06642; zf-CCH; 1.
SQ SEQUENCE 195 AA; 22297 MW; 1FEE1D8E0C2A14 CRC64;

Query Match 100.0%; Score 1013; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 9.9e-67;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSRRNPCKFEIRGCHLNGRRCHYSHNYFEWPPHALLVRQNFMLNKLKSMDSKSIDTLSH 60
DB 1 MSRRNPCKFEIRGCHLNGRRCHYSHNYFEWPPHALLVRQNFMLNKLKSMDSKSIDTLSH 60
QY 61 SGAAELDTEYALGVGVLESYIGSGINNITKQSAVCAMSKLLIENSDDIKKLDRNEEP 120
DB 61 SGAAELDTEYALGVGVLESYIGSGINNITKQSAVCAMSKLLIENSDDIKKLDRNEEP 120
QY 121 NSPKIRVNTVTSYIESNRKNKQTIHLKLPADVLKKTIKNTLDIHKSITISNPKEST 180
DB 121 NSPKIRVNTVTSYIESNRKNKQTIHLKLPADVLKKTIKNTLDIHKSITISNPKEST 180
QY 181 VNDQNDQTKNNDITG 195
DB 181 VNDQNDQTKNNDITG 195

RESULT 2

O42050_HRSV
ID O42050_HRSV PRELIMINARY; PRT; 195 AA.
AC O42050;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 27, 2005, 14:01:48 ; Search time 95.2604 Seconds
(without alignments)
688.787 Million cell updates/sec

Title: US-10-811-508-10
Perfect score: 499
Sequence: 1 MIKTKPKIMILPDKPCSI.....QFLQHLNIPEDITYTVILVS 93

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	499	100.0	93	Q6V2E5_HRSV	Q6v2e5 human respi
2	459	92.0	90	Q42047_HRSV	Q42047 human respi
3	303	60.7	90	P88812_HRSV	P88812 human respi
4	303	60.7	90	Q4KRW2_HRSV	Q4kwr2 human respi
5	173	34.7	95	Q65704_9MONO	Q65704 bovine resp
6	168	33.7	90	Q77KZ6_BRSVA	Q77kz6 bovine resp
7	168	33.7	90	Q9YS22_9MONO	Q9ys22 bovine resp
8	166	33.3	90	Q8V687_BRSVA	Q8v687 bovine resp
9	88.5	17.7	2110	Q81B35_PLAF7	Q81b35 plasmodium
10	81.5	16.3	725	Q5CHH7_CRYVO	Q5chh7 cryptospori
11	80	16.0	5074	Q7RQY0_PLAYO	Q7ryy0 plasmodium
12	79	15.8	513	Q5XC99_STRP6	Q5xc99 streptococc
13	79	15.8	513	Q99293_STRP8	Q99293 streptococc
14	79	15.8	513	Q8PI46_STRP8	Q8pi46 streptococc
15	79	15.8	513	Q8K7K2_STRP3	Q8k7k2 streptococc
16	77	15.4	409	Q568B8_BRARE	Q568b8 brachydanio
17	77	15.4	771	Q4N7R8_THEPA	Q4n7r8 theileria p
18	76	15.2	927	Q4MM00_BACCE	Q4mmo0 bacillus ce
19	75.5	15.1	502	Q4U950_THEAN	Q4u950 theileria a
20	75.5	15.1	2691	Q81LS2_PLAF7	Q81ls2 plasmodium
21	75	15.0	655	Q54BF2_DICDI	Q54bf2 dictyosteli
22	74.5	14.9	579	Q4Y024_PLABE	Q4yg24 plasmodium
23	74.5	14.9	1266	Q5CUP3_CRYPV	Q5cuf3 cryptospori
24	74	14.8	398	Q5CS38_CRYPV	Q5cs38 cryptospori
25	74	14.8	1980	Q7RF56_PLAYO	Q7rf56 plasmodium
26	73.5	14.7	207	Q21548_PHYDA	Q21548 phyllostis d
27	73.5	14.7	380	Q84KK1_PRUDU	Q84kk1 prunus dulc
28	73.5	14.7	433	Q6C1B3_YARLI	Q6c1b3 yarrowia li
29	73.5	14.7	532	Q6B8Z5_GRATL	Q6b8z5 gracilaria
30	73.5	14.7	957	Q54PW6_DICDI	Q54pw6 dictyosteli
31	73	14.6	314	Q5SKW5_ARATH	Q5skw5 arabidopsis

32 73 14.6 373 1 YSAK_CABEL Q93454 caenorhabdi
33 73 14.6 927 2 Q81WS2_BACAN Q81ws2 bacillus an
34 73 14.6 1739 2 Q81IS5_PLAF7 Q81is5 plasmodium
35 72.5 14.5 225 2 Q54AT2_DICDI Q54at2 dictyosteli
36 72.5 14.5 370 2 Q7RJX6_PLAYO Q7rjx6 plasmodium
37 72.5 14.5 989 2 Q54VC4_DICDI Q54vc4 dictyosteli
38 72 14.4 374 2 Q84KQ6_PRUMU Q84kq6 prunus mume
39 72 14.4 735 2 Q81HQ1_PLAF7 Q81hq1 plasmodium
40 72 14.4 1115 2 Q5SGQ7_DICDI Q5sgq7 dictyosteli
41 72 14.4 1401 2 Q81SD4_PLAF7 Q81sd4 plasmodium
42 71.5 14.3 228 2 Q6CWZ1_KJULA Q6cwz1 gentiana tr
43 71.5 14.3 249 2 Q689E5_GENTR Q689e5 kluyveromyc
44 71.5 14.3 626 1 HTPG_RUCBP Q89a93 buchnera ap
45 71.5 14.3 908 2 Q54DY2_DICDI Q54dy2 dictyosteli

ALIGNMENTS

RESULT 1
Q6V2E5_HRSV
ID Q6V2E5_HRSV PRELIMINARY; PRT; 93 AA.
AC Q6V2E5,
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE M2-2.
OS Human Respiratory syncytial virus 9320.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=253182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cheng X., Park H., Jin H.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY353550; RAR14268.1; -; Genomic_RNA.
DR InterPro; IPR009969; Pnemo_M2.
DR Pfam; PF07380; Pnemo_M2; 1.
SQ SEQUENCE 93 AA; 10932 MW; 344DC72B19AD7197 CRC64;

Query Match 100.0%; Score 499; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.5e-44;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MIKTKPKIMILPDKPCSISSISSESVATFNHKNILQFNHNLHNHCLNHIFDE 60
|||||
Db 1 MIKTKPKIMILPDKPCSISSISSESVATFNHKNILQFNHNLHNHCLNHIFDE 60
|||||
QY 61 IHWTQPNLLDTTQQFLQHLNIPEDITYTVILVS 93
|||||
Db 61 IHWTQPNLLDTTQQFLQHLNIPEDITYTVILVS 93
|||||

RESULT 2
Q42047_HRSV
ID Q42047_HRSV PRELIMINARY; PRT; 90 AA.
AC Q42047,
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
DE Matrix protein 2.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=B1;
RX MEDLINE=98054343; PubMed=9391135; DOI=10.1073/pnas.94.25.13961;
RA Karon R.A., Buongiorno D.A., Georgiu A.F., Whitehead S.S.,
RA Adamus J.E., Clements-Mann M.L., Harris D.O., Randolph V.B.,
RA Udem S.A., Murphy B.R., Sidhu M.S.;
RA "Respiratory syncytial virus (RSV) SH and G proteins are not essential